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(54) Title: COMPUTER SYSTEMS AND METHODS THAT USE CLINICAL AND EXPRESSION QUANTITATIVE TRAIT LOCI TO ASSOCIATE GENES WITH TRAITS

(57) Abstract: A method for associating a gene G in the genome of a species with a clinical trait T exhibited by one or more organisms in a plurality of organisms of the species. An expression quantitative trait loci (eQTL) is identified for the gene G using a first quantitative trait loci (QTL) analysis. The first QTL analysis uses a plurality of expression statistics for gene G as a quantitative trait. Each expression statistic in the plurality of expression statistics represents an expression value for gene G in an organism in the plurality of organisms. A clinical quantitative trait loci (cQTL) that is linked to the clinical trait T is identified using a second QTL analysis. The second QTL analysis uses a plurality of phenotypic values as a quantitative trait. Each phenotypic value in the plurality of phenotypic values represents a phenotypic value for the clinical trait T in an organism in the plurality of organisms. When the eQTL and the cQTL colocalize to the same locus, the gene G is associated with clinical trait T.